Evaluation of Quantitative and Qualitative Characteristics of some Walnut Genotypes in Kermanshah Province

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ABSTRACT

Shafaei, Z., and Arzani, K. 2016. Evaluation of quantitative and qualitative characteristics of some walnut genotypes in Kermanshah province. **Seed and Plant Improvement Journal 32-1:** 437-459 (in Persian).

Iran is known as one of the main centers of diversity and cultivation of walnut in the world. This diversity can be considered in breeding programs. In a walnut breeding program, identification and selection of superior genotypes is an important task. This research was conducted to identify superior genotypes within the walnut populations grown in some parts of Kermanshah province during 2013-2015. Some phenological and pomological traits of 59 walnut genotypes were evaluated according to UPOV and IBPGR descriptors. Based on the obtained results, the average nut weight, kernel weight and kernel percentage were 9.31-22.35g, 4.34-11.20g and 36.91-68.29%, respectively. The highest kernel percentage (68.28) belonged to genotype Kh86. Genotype Kh65 had the highest nut weight (22.35g) and kernel weight (11.20g). Genotype Kh110 with 25 days delay in leafing in compare to the reference standard, was considered as a late leafing genotype. Genotypes Ks33 and Kh128 showed the highest percentage of homogamy (100%). The 59 studied genotypes were classified in to five clusters by cluster analysis. Finally, genotypes Kh153, Kh150, Kh149, Kh146, Kh134, Kh128, Kh127, Kh110, Kh88, Kh87, Kh86, Kh70, Kh69 Kh65, Ks42, Ks39, Ks35 and Ks29, that had better characteristics of nut and kernel, were recognized as promising genotypes.

Key words: Walnut, promising genotypes, pomological traits, phonological traits, cluster analysis.

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Tolerance to the Late Spring Frost in some Quince (*Cydonia oblonga* Mill.) Genotypes in Karaj Climate

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ABSTRACT

Mohammadi, M., Nadi, S., and Abdollahi, H. 2016. Tolerance to the late spring frost in some quince (*Cydonia oblonga* Mill.) genotypes in Karaj climate. **Seed and Plant Improvement Journal 32-1:** 461-477 (in Persian).

Among various species of pome fruits, quince trees are considered as a late blooming species, however late spring frosts cause damage on flower buds in some years. Damage level caused by a -8ºC spring frost occurred in the mid-April of 2014 in Karaj were evaluated on 36 five years old quince genotypes grown in the collection garaden of Kamalshahr before bud burst stage. The evaluated genotypes had been collected from Khorasan Razavi, Isfahan, Guilan, Ardabil and Tehran provinces. Based on the results, the highest levels of spring frost damage (10 up to 80%) were recorded on the genotypes originated from low altitudes of Isfahan, Khorasan and Guilan provinces, while the frost damage was not observed on the genotypes originated from high altitudes of these provinces. Correlation analysis of evaluated characteristics of the genotypes revealed the highest negative correlation between length of bud flower and level of frost damage, while severity of frost damage had not significant correlation with tree yield and final fruit size of the genotype. Regarding the results of this investigation, it seems that for introduction of new quince cultivars for regions with late chilling damages on the flower buds, the genotypes originated from Ardebil are more suitable. The quince genotypes of Ardebil demonstrated high fruit quality and late blooming period that could be considered as useful traits in selection and breeding of quinces.

Key words: Quince tree, genotypes, morphology, genetic diversity, cold damage.

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Response of some Chickpea Genotypes to Races of *Ascochyta rabiei* Cause of Ascochyta Blight in Greenhouse

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ABSTRACT

Shahriari, D., Torabi, M., and Kangarloo, S. 2016. Response of some chickpea genotypes to races of *Ascochyta rabiei* cause of ascochyta blight in greenhouse. **Seed and Plant Improvement Journal 32-1:** 479-488 (in Persian).

Ascochyta blight caused by *Ascochyta rabiei* (Pass.) Lab. is an important disease of chickpea in Iran and worldwide. Information about the races of the pathogen in different areas is necessary for improvement of resistant cultivars. In the present study physiologic races of 28 isolates of *A. rabiei* collected from five areas of Kermanshah province of Iran during 2013 and 2014, were determined using seven chickpea standard differential cultivars. Six different races were identified. Race 1 with seven isolates(25%), race 2 with five isolates (17.8%), race 3 with seven isolates (25%), race 4 with four isolates(14.4%), race 5 with two isolates (7.2%) and race 6 with three isolates (10.6%) were the prevatent races in Kermanshah province. Races 1, 2, 3 and 4 with 23 isolates (82.1%) were distributed all over areas of the province, while race 6, the highly virulent isolate, was detected only in a restricted area in Sararood. Response of 48 genotypes of including improved cultivars, advanced chickpea lines and landraces were evaluated against the six identified races in greenhouse. The results showed that most of the genotypes were susceptible or highly susceptible to different races. Recently released cultivars, Adel and Azad, were moderately resistant to the highly virulent race 6 and resistant to the other races. The remaining genotypes were susceptible or highly susceptible to this race. Based on the results of this study, in addition to Adel and Azad cultivars, lines Flio 51-87-3c, ILC-3274 and LMR-165 which were resistant or moderately resistant to the most prevalent races 1, 2, 3 and 4, can be also recommended as resistant sources for the region.

Key words: Chickpea, cultivars and lines, ascochyta blight, races, resistance.

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Genetic Diversity of Grain Yield and some Morphological Traits in Local Bread Wheat Lines

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ABSTRACT

Arzhang, S., Bernosi, I., Abdollahi Mandolakoni, B., and Hassanzadeh Ghoorttappeh, A. 2016. Genetic diversity of grain yield and some morphological traits in local bread wheat lines. **Seed and Plant Improvement Journal 32-1:** 489-506 (in Persian).

To assess the genetic variability of grain yield, yield components and some morphological traits in 99 bread wheat lines deriven from local genotypes, an experiment was carried out based on randomized complete block design with three replications during the 2010-11 and 2011-12 cropping seasons at Saatlou Station of Agricultural and Natural Resources Research Center of Urmia and at Research Field of Urmia University. Analysis of variance for biological yield and grain yield showed significant differences among lines in both years. The highest biological and grain yield belonged to line No. 18 and line No. 87, respectively. Combined analysis of variance indicated significant differences among interactions between lines and years for all studied traits except awn length, number of spikelets/spike and number of grains/spike ($P<0.01$). Cluster analysis based on mean traits using Ward's method assigned the lines into seven groups. Similarity between results of multivariate analysis of variance and cluster analysis was observed for classification of lines. Discriminant function analysis revealed that 88.9% of the grouping was correct. Groups 1 and 6 had the maximum mean of grain yield and yield components. In addition, the first three canonical functions explained 80.3% of the total variance. Canonical discrimination coefficients for these three functions indicated that grain yield, biological yield, spike length, plant height, thousand grain weights, flag leaf weight, flag leaf width, spike density and days to flowering were the most important for discriminating among wheat lines.

Key words: Bread wheat, canonical discriminant analysis, cluster analysis, genetic diversity.

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Genetic Diversity of some Populations of Watermelon (*Citrullus lanatus* var. *lanatus*) Based on Morphological Traits and Microsatellite Markers (ISSR)

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ABSTRACT

Nohtani, H., Masoumiasl, A., Sabbagh, S. K., and Amiri Fahliani, R. 2016. Genetic diversity of some populations of watermelon (*Citrullus lanatus* var. *lanatus*) based on morphological traits and microsatellite markers (ISSR). **Seed and Plant Improvement Journal 32-1:** 507-525 (in Persian).

For assessing the genetic diversity of Iranian populations of watermelon, 24 local populations together with one foreign cultivar (F-1 hybrid of Sakata Company) were studied using morphological traits and ISSR markers. Populations were grown in field in a randomized complete block design with three replications, and then morphological traits including fruit number in bush, the tallest banch length, fruit weight, fruit diameter and length and rind thickness were measured. Results of analysis of variance showed significant differences among all populations regarding the morphological traits. Cluster analysis based on morphological traits, divided populations in to four groups. In assessment of genetic diversity by molecular markers, ten used primers generated 87 scorable bands, which 75 sites were polymorphic. Polymorphic information content (PIC) of primers varied from 0.52 (marker P4) to 0.91 (marker UBC864) with anaverage of 0.83. Cluster analysis based on Jaccard genetic similarity coefficient, placed populations into seven main clusters. Minimum and maximum genetic distances were observed between populations of Kordestan and Kermanshah and Mazandaran and Khorasan, respectively. Generally the results of this study revealed that ISSR can be efficiently used for assessment of genetic diversity in watermelon populations native to Iran and UBC823 and UBC864 were recognized as the best primers forfiture studies.

Key words: Watermelon, populations, genetic diversity, ISSR markers.

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Genetic Diversity in Safflower Germplasm of National Plant Gene Bank of Iran

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ABSTRACT

Abbasali, M., and Zahravi, M. 2016. Genetic diversity in safflower germplasm of National Plant Gene Bank of Iran. **Seed and Plant Improvement Journal 32-1:** 527-542 (in Persian).

Safflower is the most suitable crop plant for oil production in dry areas and regarding the fact of climate change, it has been come in consideration in recent years. A broad genetic base and rich germplasm is necessary for breeding of this crop. This research was performed in 2011 to investigate variability of safflower germplasm. A total of 345 accessions of safflower collection of National Plant Gene Bank of Iran were planted and evaluated in research field of Seed and Plant Improvement Institute in Karaj. Preliminary evaluation showed that many accessions consisted of several diverse morphotypes, hence, by isolating and morphotype determination, the number of accessions reached to 534, which were investigated in an observational design. The results indicated that corolla color and spine intensity of outer involucral bracts had considerable amount of Shannon index. The highest (85.62) and the lowest (7.24) coefficient of variation belonged to seed weight of single plant and days to flowering, respectively. The first three principal components justified 56.13% of variation, the first one emphasized on yield components and the second on vegetative traits. The accessions were located in five groups by K means clustering method. Distribution of country origin of the accessions was consistent with their geographical situation in some cases. Totally, results showed that the studied accessions have a considerable variation which could be exploited in breeding programs.

Key words: Safflower, National Plant Gene Bank of Iran, morphotype, accession.

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Evaluation of Yield Related Traits in Sugar Beet Multigerm Hybrids Resistant to Rhizomania Disease

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ABSTRACT

Vahedi, S., Shahbazi, H., Bazrafshan, M., Noshad, H., and Fasahat, P. 2016. Evaluation of yield related traits in sugar beet multigerm hybruds resistant to rhizomania disease. **Seed and Plant Improvement Journal 32-1:** 543-556 (in Persian).

Rhizomania disease is one of the most destructive diseases of sugar beet in most sugar beet planting areas throughout the world. The disease widespread in some provinces in Iran, necessitates the development of new resistant hybrids and their commercially usage. In this study, new hybrids were developed from a cross between five pollinators bearing Rz_1 gene and three single-crosses (276-3.27×SB36, 276-37.34×SB36, and I13×A37.1) in 2010. Developed hybrids were evaluated in an infected field to rhizomania in Fars province. Later, hybrids together with resistant and susceptible controls were evaluated in two locations of Mashhad and Karaj in 2011 and 2012. Two-years experiment r esults showed that (I13×A37.1)×S1-88239, (276-3.27×SB36)×S1-88239, and (276-37.34×SB36)×S1-88239 hybrids had better response in terms of yield and qualitative traits compared to resistant control and other hybrids. Based on the results of this experiment, pollinator S1-88239 can be also recommended for the development of resistant cultivars to rhizomania in the target areas.

Key words: Sugar beet, rhizomania, resistance evaluation, resistant hybrids, yield.

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Analysis of Yield Stability of some White Bean (*Phaseolus vulgaris* L.) Genotypes using AMMI Method

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ABSTRACT

Kooshki, M. H., Ghaedrahmati, M., Assadi, B., Kamel, M., Khorshidi Benam, M. B., and Dorri, H. R. 2016. Analysis of yield stability of some white bean (*Phaseolus vulgaris* L.) genotypes using AMMI method. **Seed and Plant Improvement Journal 32-1:** 557-573 (in Persian).

Genotype × environment interaction effects have important roll in superior genotypes selection. To study genotype, environment and genotype × environment effects on seed yield, twelve white bean genotypes were evaluated in a randomized complete block design with three replications at four locations (Broujerd, Zanjan, Khomein and East Azarbaijan)for two years (2012-2014). Results of combined variance analysis showed significance of genotype, environment and genotype × environment effects on seed yield. The highest and lowest seed yield of genotypes were obtained in Broujerd (4335 $kgha^{-1}$) and Khomein (1354.2 $kgha^{-1}$) stations, respectively. Analysis of AMMI variance showed that six IPCAs were significant and seventh IPCA was considered as noise. Genotype × environment interaction effect was more important than main effect of genotype. First two main components explained 71% of total yield variance. According to values of first significant main component (PCA1), AMMI stability value (ASV) and genotype stability index (GSI), genotype 11805/DANESHKADEHwas known as the most stable genotype with high yield.

Key words: White bean, genotypes, genotype × environment effect, AMMI stability value (ASV), Genotype stability index (GSI).

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